

WHAT IS CLAIMED IS:

1. A method for preparing amplification products useful for forming an array of polynucleotides that is representative of a plurality of first polynucleotides comprising:
- 5 a) providing a plurality of samples of double-stranded polynucleotide fragments, wherein each sample is derived from a first polynucleotide;
- 10 b) ligating adapters to each end of the polynucleotide fragments to produce modified polynucleotide fragments, wherein each adapter comprises a first strand and a second strand, the second strand having a region of substantial complementarity to a region of the first strand;
- 15 c) amplifying the modified polynucleotide fragments to produce an amplification product for each sample of polynucleotide fragments;
- d) isolating each amplification product; and
- e) resuspending each amplification product to form a target solution suitable for application to a substrate to produce an array of polynucleotides.
2. The method of Claim 1 additionally comprising applying the target solutions to one or more substrates, wherein each target solution is applied to a distinct location on one substrate and/or target solutions are applied to different substrates that are combined to produce an array of polynucleotides.
- 20 3. The method of Claim 1 wherein the double-stranded polynucleotide fragments are derived from a polynucleotide library.
4. The method of Claim 3 wherein the polynucleotide library is a genomic DNA library.
5. The method of Claim 3 wherein the polynucleotide library is a cDNA library.
- 25 6. The method of Claim 3 wherein the double-stranded polynucleotide fragments are derived from YAC, BAC, P1 or PAC clones.

7. The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 50 kilobases.
8. The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 100 kilobases.
- 5 9. The method of Claim 7 wherein the first polynucleotides each have a complexity of less than about 500 kilobases.
10. The method of Claim 1 wherein the double-stranded polynucleotide fragments are obtained using one or more restriction endonucleases.
11. The method of Claim 1 wherein the average length of the double-stranded polynucleotide fragments is less than about 5 kilobases.
- 10 12. The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is less than about 2 kilobases.
13. The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is greater than about 100 basepairs.
- 15 14. The method of Claim 2 wherein the average volume of each target solution applied to the substrate is less than about 2 nanoliters.
15. The method of Claim 14 wherein the average volume of each target solution applied to the substrate is equal to greater than about 0.002 nanoliters.
16. The method of Claim 2 wherein the array comprises at least 1000 amplification products in a 1 cm² region of substrate.
17. The method of Claim 2 wherein the target solutions are robotically spotted on the substrate.
18. The method of Claim 2 wherein at least one strand of the adapters includes an amino group.
- 25 19. The method of Claim 1 wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume.

Sub
B5

20. An array of polynucleotides that is representative of a plurality of first polynucleotides wherein said array is produced according to the method of Claim 2 and comprises at least 1000 amplification products in a 1 cm² region of substrate.
21. A plurality of target solutions prepared according to the method of Claim 3.
- 5 22. The plurality of target solutions of Claim 21 wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume.

09574386-051900